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Argyrin B a non-competitive inhibitor of the human immunoproteasome exhibiting preference for β 1i

Running title:

Argyrin B an inhibitor of the immunoproteasome

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Abstract

Inhibitors of the proteasome have found broad therapeutic applications however, they show severe toxicity due to the abundance of proteasomes in healthy cells. In contrast, inhibitors of the immunoproteasome, which is upregulated during disease states, are less toxic and have increased therapeutic potential including against autoimmune disorders. In this project, we report argyrin B, a natural product cyclic peptide to be a reversible, non-competitive inhibitor of the immunoproteasome. Argyrin B showed selective inhibition of the $\beta 5i$ and $\beta 1i$ sites of the immunoproteasome over the $\beta 5c$ and $\beta 1c$ sites of the constitutive proteasome with nearly 20-fold selective inhibition of $\beta 1i$ over the homologous $\beta 1c$. Molecular modelling attributes the $\beta 1i$ over $\beta 1c$ selectivity to the small hydrophobic S1 pocket of $\beta 1i$ and $\beta 5i$ over $\beta 5c$ to site-specific amino acid variations that enable additional bonding interactions and stabilization of the binding conformation. These findings facilitate the design of immunoproteasome selective and reversible inhibitors that may have a greater therapeutic potential and lower toxicity.

Keywords

Immunoproteasome, selective inhibitors, argyrin B, non-competitive binding, docking

Introduction

Protein degradation is involved in the regulation of key pathways such as cell cycle control, DNA repair and apoptosis, where the ubiquitin-proteasome system is the main pathway for the degradation of cytosolic proteins deemed redundant, misfolded or toxic (Ciechanover, 2005; Suh et al., 2013). The 20S core of the proteasome contains the three proteolytic sites through which proteins are cleaved into oligopeptides by the chymotrypsin- ($\beta 5$) trypsin- ($\beta 2$) and caspase- ($\beta 1$) like activities (Heinemeyer, Ramos, & Dohmen, 2004; Orlowski & Wilk, 2000). Inhibitors of the proteasome act in one or more of the active sites and have shown broad therapeutic applications, particularly for multiple myeloma and mantle cell lymphoma. However, since the proteasome is required for normal cell function its inhibition becomes associated with severe toxicity (Crawford, Walker, & Irvine, 2011; Genin, Reboud-Ravaux, & Vidal, 2010; Goldberg, 2012; Alexei F. Kisselev, van der Linden, & Overkleeft, 2012; Kuhn et al., 2007; Moore, Eustáquio, & McGlinchey, 2008; Parlati et al., 2009; Pellom & Shanker, 2012; Shah, Biran, & Vesole, 2016; Shivakumar & Jagganath, 2006; Sun et al., 2015; Teicher & Tomaszewski, 2015; Wu et al., 2010; Zhang et al., 2016, 2014). Cells in disease states, where the demand for protein degradation is higher, are capable of producing immunoproteasomes in which the catalytic $\beta 1c$, $\beta 2c$ and $\beta 5c$ subunits of the constitutive proteasome are replaced by the homologous $\beta 1i$, $\beta 2i$ and $\beta 5i$ while all other subunits remain unchanged (Kniepert & Groettrup, 2014; Yewdell, 2005). As a result of these structural changes the cleavage specificities of the immunoproteasome and constitutive proteasome differ and immunoproteasome preferentially cleaves after hydrophobic amino

acids(Gaczynska, Rock, Spies, & Goldberg, 1994). Besides the constitutive proteasome and immunoproteasome two additional intermediate subtypes exist, which contain a mixture of constitutive and immunoproteasome subunits i.e either immunosubunit $\beta 5i$, and constitutive subunits $\beta 1ic$ and $\beta 2c$, or immunosubunits $\beta 1i$ and $\beta 5i$, and constitutive subunit $\beta 2c$. Intermediate proteasomes are abundant in normal tissues (between one-third and one-half of total proteasome content) and are also present in human tumor cells (10-20%) and dendritic cells (30-50%) and exhibit trypsin and chymotrypsin-like activities that are in-between those of the constitutive and the immunoproteasome. As such, intermediate proteasomes produce a unique set of antigenic peptides and together with the immunoproteasome they represent valuable targets for cancer immunotherapy (Dahlmann, Ruppert, Kuehn, Merforth, & Kloetzel, 2000; Guillaume et al., 2010, 2012; Vigneron & Van den Eynde, 2014).

Most existing proteasome inhibitors block the active sites of both the constitutive proteasome and immunoproteasome at similar potencies(Bakas et al., 2018; Kuhn & Orłowski, 2012; Parlati et al., 2009). However, significant advancements in crystal structure elucidations have enabled the identification of sufficient structural differences in the binding pockets of the different forms of proteasomes (Groll, Berkers, Ploegh, & Ovaa, 2006; Harshbarger, Miller, Diedrich, & Sacchettini, 2015; Huber et al., 2012)(Santos et al., n.d.) to allow for selective structure-based drug design and selective inhibition. These structural differences have allowed the design of peptide epoxyketone derivatives (Ho, Bargagna-Mohan, Wehenkel, Mohan, & Kim, 2007) (Carmony et al., 2012), and peptidyl boronate ML604440(Basler et al., 2012) that bind

specifically at the β 1i site. Furthermore, oxathiazolones have been reported to inhibit β 5i with a remarkable 4700-fold selectivity over the constitutive proteasome (Fan, Angelo, Warren, Nathan, & Lin, 2014). Peptide epoxy-ketones represent another class of β 5i selective inhibitors (de Bruin et al., 2014; Dubiella et al., 2014; Fan et al., 2014; Groll, Korotkov, Huber, de Meijere, & Ludwig, 2015; Koroleva et al., 2015) among which PR-957, an analogue of carfilzomib, shows 20 to 40-fold selectivity towards β 5i in MOLT-4 cells where both forms of the proteasome are expressed and showed evidence of disease reversal of rheumatoid arthritis mouse models (Muchamuel et al., 2009). PR-924, a selective inhibitor of the immunoproteasome with up to 250-fold selectivity towards β 5i over β 5c (Huber, Heinemeyer, de Bruin, Overkleeft, & Groll, 2016) selectively inhibited growth and triggered apoptosis in multiple myeloma cells over normal cells, validating the β 5i site as a target for multiple myeloma treatment (Singh et al., 2011). These inhibitors are irreversible and covalently modify the active site threonine forming a protein-drug adduct. Landsteiner and Jacobs over 80 years ago (Landsteiner & Jacobs, 1935) discovered a direct association between a chemical's propensity to bind covalently to protein and immune sensitization with the risk of developing idiosyncratic adverse drug reactions (IADR) (Zhou, Chan, Duan, Huang, & Chen, 2005). From this perspective, reversible inhibitors can offer an advantage as they can potentially inhibit at low nanomolar concentrations without producing protein adducts that trigger drug hypersensitivity. Recently, reversible β 5i selective inhibitors have been reported to selectively induce cell death in malignant myeloma cells (Santos

et al., n.d.) and to promote long-term acceptance of cardiac allografts in mice by regulating immune activity(Sula Karreci et al., 2016).

Argyriins are a family of cyclic peptides derived from the myxobacterium *Archangium gephyra* analogues of which have shown to be potent, reversible inhibitors of the constitutive proteasome with mechanisms distinct to existing therapeutics(Bülow et al., 2010; Ferrari et al., 1996; Loizidou & Zeinalipour-Yazdi, 2014; Selva et al., 1996; Stauch et al., 2010). Argirin B (Figure 1), initially discovered in screening for antibiotics, has displayed some antibacterial as well as antifungal activities(Nyfeler et al., 2012). In human B cells, argirin B exhibited immunoglobulin G inhibition and showed reduced activity of T and B lymphocytes in murine studies, highlighting its strong immunosuppressive effects(Sasse et al., 2002). Taking into consideration both the proteasome inhibition as well as immunosuppressive effects of argirin B, in this project we wished to further investigate the potential for selective inhibition of the immunoproteasome. Active site inhibition of the $\beta 5c$, $\beta 1c$ subunits of the constitutive proteasome and the $\beta 5i$, $\beta 1i$ subunits of the immunoproteasome were investigated using purified enzyme assays alongside molecular modelling. Kinetic assays revealed that argirin B selectively inhibits $\beta 1i$ over $\beta 1c$ with 20-fold selectivity and shows low micromolar K_i values for both $\beta 1i$ and $\beta 5i$. Molecular modeling simulations reveal that the increased hydrophobicity and smaller size of the $\beta 1i$ S1 pocket contributes to the selective binding of argirin B while the site specific amino acid variation A27S (from $\beta 5c$ to $\beta 5i$) enables additional hydrogen bonding at the $\beta 5i$ site that may further stabilize binding compared to $\beta 5c$.

Materials and methods

Material

20S proteasome (purified human erythrocyte), 20S immunoproteasome (purified human enzyme), NBS 96-well microplates, 7-amino-4-methylcoumarin (AMC) standards, Z-Leu-Leu-Glu-AMC, Suc-Leu-Leu-Val-Tyr-AMC, epoxomicin, sodium dodecyl sulfate (SDS) and vinyl sulfone (Ada-(Ahx3)-(Leu)3-vinyl sulfone) were purchased from Enzo Life Sciences, Exeter UK. Ac-Pro-Ala-Leu-AMC was purchased from BioTechne Abingdon, UK, dimethyl sulfoxide (DMSO) from Fisher Scientific, Loughborough, UK and Argyrin B was a donation from Novartis.

Purified enzyme assays

Substrate and inhibitor reagents were dissolved in DMSO for stock solutions and subsequently diluted in proteasome assay buffer to desired concentrations. Assay reagents were added to 96-well plates to a final volume of 50 μ l per well, throughout. Concentrations of the 20S proteasome and 20S immunoproteasome were maintained constant at 0.1 μ g/well. AMC standards were prepared from a 1:2 serial dilution of 8 μ M to 0.25 μ M and blank. All purified enzyme reactions were performed at 37 °C and the liberation of AMC was measured over time using a BMG Labtech fluorescence plate reader set at 355/460 nm (excitation/emission). Positive controls were performed by the reaction of proteasome or immunoproteasome with active site specific substrates: Z-LLE-AMC (β 1), Ac-PAL-AMC (β 1i) and Suc-LLVY-AMC (β 5/ β 5i). Negative controls were performed using epoxomicin a potent inhibitor of β 5/ β 5i and vinyl sulfone a potent inhibitor of β 1/ β 1i. Blanks were performed with substrate only and additional controls for solvent (DMSO) concentration were used where applicable.

Using 0.1 $\mu\text{g}/\text{well}$ of enzyme, a range of at least 7 substrate concentrations were used to generate Michaelis-Menten plots for Michaelis-Menten constant (K_m) analysis at each active site. Subsequent K_m values were used as the single substrate concentration in IC_{50} plots that covered a logarithmic range of at least 10 argyris B concentrations. For kinetic assays to determine inhibition constant (K_i), the following inhibitor and substrate concentrations were used: argyris B concentrations ranged from estimated IC_{50} value ($\beta_{1c} = 183.7 \mu\text{M}$, $\beta_{1i} = 10.4 \mu\text{M}$, $\beta_5 = 11.4 \mu\text{M}$, $\beta_{5i} = 10.3 \mu\text{M}$) $\times 0, 0.33, 1$ and 3 , whilst substrate concentration covered K_m ($\beta_1 = 95.4 \mu\text{M}$, $\beta_{1i} = 69.9 \mu\text{M}$, $\beta_5 = 72.4 \mu\text{M}$, $\beta_{5i} = 89.8 \mu\text{M}$) $\times 2.5, 1.25, 0.625, 0.3125$ and 0.15625 .

Assays were performed with triplicates at every control and concentration variant. For each replicate, the initial rate of reaction was determined from the linear phase of the graph at which less than 10% of substrate had been consumed. GraphPad Prism 6 non-linear curve fitting analysis was used for calculation of K_m , IC_{50} and K_i values. For K_m a Michaelis-Menten plot as the preferred model, whilst for IC_{50} analysis, a normalised response curve was fit against logarithmic inhibitor concentration allowing for variable slope function. Data are reported with mean, SEM and 95% confidence interval. A standard, unpaired, t-test was used to analyse significance between the 3 IC_{50} value repeats of argyris B at different active sites at 95% confidence level.

Alongside K_m and V_{max} values, Akaike's information criterion (AICc)(Motulsky & Christopoulos, n.d.) and the F test hypothesis testing approach at $p < 0.05$ were used to determine the best-fit simultaneous non-linear regression analysis model between competitive, non-competitive, uncompetitive and mixed inhibition that subsequently calculated K_i . Estimates of the inhibition

constant K_i are reported with SEM and 95% confidence intervals.

Computational methods

All 3-dimensional structures were obtained from RCSB Protein Data Bank and prepared using the molecular graphics package PyMOL (v1.7.4.5). An argyirin B structure was isolated from PDB:4FN5(Nyfeler et al., 2012) and its geometry optimised using the Molecular Mechanics with UFF force field function of Avogadro(Hanwell et al., 2012). The Human constitutive 20S proteasome structural data was available from PDB:4R3O(Harshbarger et al., 2015). $\beta 1$, $\beta 2$ and $\beta 5$ active sites were cut for residues within 28 Å from the catalytic Thr1 position of each active subunit chain from the same β -ring on the same monomer using PyMOL. IP structural data was obtained from PDB:3UNH(Huber et al., 2012) murine IP and subsequently modified in order to create a humanised IP model as follows: human active site sequences for $\beta 1i$, $\beta 2i$ and $\beta 5i$ (UniProt: P28065, P40306, P28062, respectively) were aligned to murine immunoproteasome FASTA sequences using EMBL-EBI ClustalOmega, EMBOSS Smith-Waterman alignment algorithm followed by identification of the conserved amino acids. Subsequently, the amino acid mutation utility of SwissPDB viewer (v.4.10) was used to mutate variable, individual amino acids of murine IP to those of the corresponding human IP. Active sites were subsequently cut as described for the constitutive proteasome.

AutoDock (v.4.2.6) was used to simulate argyirin B binding(Morris et al., 2009) at the active sites of the immunoproteasome and constitutive proteasome. The grid box was set at 70x, 70y, 70z dimensions, centred based on Thr1 co-ordinates on the active subunit chains as follows: 23.238, -78.082, -11.152 for

$\beta 1i$, 52.961, -24.734, -1.942 for $\beta 5i$ and -44.697, 77.350, -80.590 for $\beta 1c$, -42.794, 25.372, -104.397 for $\beta 5c$.

Argyirin B was allowed rotational freedom at the bonds connecting the tryptophan rings to the peptide cycle, as well as the Trp2-OMethoxy bond while the constitutive proteasome and immunoproteasome active sites were treated as non-flexible. A genetic algorithm with 50 runs was selected for all docking experiments. Each docking experiment was repeated 10 times and for each set of 10 replicate best binding energies, the data were tested for normality where those with $p > 0.05$ show normal distribution. For normally distributed sets, equal variance was tested between each active site. A 2-sample t-test was used for those of equal variance, whilst a non-parametric Mann-Whitney test was used for results not of equal variance, to test for significance (p -values of < 0.05 show statistical difference).

Results

Kinetic assays

To assess the inhibitory activity of argyirin B against the immunoproteasome we performed kinetic assays using recombinant proteasome and immunoproteasome and $\beta 1c$, $\beta 1i$, $\beta 5c$ and $\beta 5i$ site-specific substrates (Miller, Ao, Kim, & Lee, 2013). The $\beta 2c$ and $\beta 2i$ sites were excluded from testing since as revealed by the crystal structures their active sites are remarkably similar and thus a difference in the binding affinity of inhibitors towards $\beta 2c$ and $\beta 2i$ is not expected (Huber et al., 2012). To determine the IC_{50} values (Figure 2) the substrate concentration was chosen at the K_m value in order to avoid unrepresentative values from different inhibition modes (Cheng & Prusoff, 1973) (Michaelis-Menten plots shown in Figure S1 in Supporting

information). The highest binding affinity that argyrin B achieved was for the $\beta 5i$ site with an IC_{50} of 3.54 μM , followed by $\beta 5c$ and $\beta 1i$ with IC_{50} of 8.30 μM and 8.76 μM , respectively. The affinity of argyrin B for the $\beta 1c$ site was much lower with IC_{50} of 146.5 μM , showing a 16-fold selectivity towards $\beta 1i$ over $\beta 1c$ (**Table 1**). Kinetic analysis further supported our data where the K_i for the $\beta 1c$ site was estimated to be larger than 100 μM (**Table 1**). An accurate value for the K_i for $\beta 1c$ could not be determined due to the high concentration of argyrin B at 3 x IC_{50} (439.5 μM) that was required to carry out the $\beta 1c$ K_i range tests. At this concentration the amount of DMSO that is required to dissolve argyrin B is high enough to have a significant impact on enzyme-substrate reaction. Kinetic analysis revealed similar inhibition constants for $\beta 1i$ and $\beta 5i$ with estimated K_i 5.21 and 6.61 μM , respectively, followed by $\beta 5c$ with K_i 13.85 μM . Over 20-fold selectivity of $\beta 1i$ over the $\beta 1c$ site is observed. K_i values were determined based on a non-competitive model, which proved to be the best fit based on AICc analysis(Kakkar, Pak, & Mayersohn, 2000). The non-competitive model and estimated K_i values were also supported by alternative analysis methods including Cornish-Bowden and Dixon plots as well as a conventional Hanes-Woolf plot (Figure S2-S5).

Despite inhibiting non-competitively, argyrin B can still bind at the active site as reported for other members of the argyrin family(Loizidou & Zeinalipour-Yazdi, 2014; Stauch et al., 2010) as well as the $\beta 5c$, $\beta 5i$ asparagine-ethylenediamine-based inhibitors(Santos et al., n.d.). Non-competitive binding can potentially be beneficial in a cell environment where protein degradation is inhibited leading to progressive accumulation of substrate, as the concentration of substrate would not influence the degree of inhibition.

Molecular docking

Molecular docking was employed to shed light on the possible mechanisms of selective inhibition exhibited by argyrin B towards the immunoproteasome.

Based on existing knowledge that argyrin analogues bind near the active site of the proteasome (Stauch et al., 2010), the grid box was centered at the $\beta 1i$, $\beta 5i$ and $\beta 1c$, $\beta 5c$ active sites for the molecular docking studies with argyrin B.

The active sites were simulated by using the three-dimensional structure for the human constitutive proteasome and a homology model of the human immunoproteasome that was generated using the crystal structure of the mouse immunoproteasome as the template (Figure S6, S7 and Table S1).

Compared to the $\beta 1c$ active site, $\beta 1i$ is smaller in size and has a more hydrophobic character. This is exemplified by the key substitutions from constitutive to immunoproteasome in residues of the S1 specificity pocket, T22V, T33F, R47L, T52A (Figure 3). Apart from the conservative R47L substitution, all others involve changing of a polar amino acid to a hydrophobic amino acid and as such, provide a hydrophobic character. Additionally, the $\beta 1i$ site is short of one amino acid, at position 115, which is consistent with the reported sequences for $\beta 1i$ (Huber et al., 2012).

The binding of argyrin B at both $\beta 1i$ and $\beta 1c$ sites was found to be mainly driven by VdW, hydrogen bonding and desolvation interactions with argyrin B displaying a significant difference in binding preference towards $\beta 1i$ (-11.83 kcal/mol) compared to $\beta 1c$ (-10.12 and -9.74 kcal/mol). One main binding conformation was identified at the $\beta 1i$ site showing great consistency of interactions between argyrin B and amino acids of the $\beta 1i$ active site. Argyrin B is positioned close to Thr1, which participates in two hydrogen bonding

interactions with the thiazole nitrogen of argyrin B as well as an additional hydrogen bond with the adjacent carbonyl oxygen. The latter is further stabilized by a hydrogen bond with Ser129. Additional hydrogen bonding were identified between trp 1 of argyrin B and Ser46 as well as between an amide backbone of the argyrin macrocycle and Val 20. VdW interactions were identified between argyrin B and the amino acids Ala49, Arg19, His97, Met5, Ser48, Val20, Gly128, Gly47, Ala96, Leu115 and Tyr30. Additionally, Ser95 is likely to be involved in dipole-dipole interactions with trp 2 of argyrin B. In contrast, molecular modeling suggested a dual binding mode for argyrin B at the active site of β 1c, where interactions with residues Arg35, Gly47, Met116, and Met95, appear in both conformations. The two binding conformations appear at a 2:3 ratio. At the more abundant binding *conformation 1* (Fig. 3C,D) argyrin B is positioned close to Thr1 forming a similar hydrogen bond with the thiazole ring which is further stabilized through a second hydrogen bond with Gly47. Additional hydrogen bonding interactions were identified between the amino acids Thr22 and backbone carbonyl of argyrin B as well as Met116 and trp2. Trp1 is surrounded by residues Arg35, Gly97, Gly129, Ser130 and Ser46 forming VdW interactions. Additional VdW interactions were between the amino acids Thr20, Thr21, Gly23, Ala49, Met95, and Val20 and the cyclic backbone of argyrin B.

In the less frequently occurring but more energetically favored (-10.12 kcal/mol compared to -9.74 kcal/mol) *conformation 2*, argyrin B is positioned further away from Thr1 enabling aromatic interactions between Tyr30 and the tryptophan rings of argyrin B (Fig. 3E-F). Hydrogen bonding interactions are observed with amino acids Arg35, Gly97, and Gly128 and VdW interactions

with amino acids Gly129, Pro115, Met116, Gly47, Met95, Met5, Tyr30, Leu33, Ser133, at β 1c.

Overall there are 5 hydrogen-bonding interactions in β 1i compared to 4 hydrogen-bonding interactions in β 1c *conformation 1*, offering the extra stabilisation. It is likely that the more compact size of the β 1i site compared to the β 1c allows for a better fit for argyrin B and the facilitation of interactions with amino acids of the active site. On the other hand, the more spacious β 1c site allows argyrin B to adopt several binding conformations and this is exemplified by the two main binding modes identified by molecular modelling. Similarly to the β 1 sites, the binding of argyrin B at both β 5i and β 5c sites was found to be mainly driven by VdW, hydrogen bonding and desolvation interactions. One main binding conformation was identified at the β 5i site showing great consistency of interactions between argyrin B and amino acids of the β 5i active site (Figure 4A,B). Four main hydrogen-bonding interactions were identified with residues Thr1, Ser21 and Ser46. VdW interactions were identified with amino acids Val31, Ala49, Met45 and Lys33, which surround trp1 of argyrin B as well as amino acids Gly47, Gly129 and Tyr169. A dual binding mode was identified at the β 5c site of the constitutive proteasome. In β 5c, the frequency of appearance of the two main conformations follows a similar pattern to β 1c, that is a 2:3 ratio for β 5c *conformation 1* (binding energy -10.52 kcal/mol) vs β 5c *conformation 2* (binding energy – 10.72 kcal/mol) where both conformations show similar binding energies. In both binding conformations argyrin B binds in a similar area but the tryptophan rings are positioned on opposite sites (Figure 4C-F). In *conformation 1* (Figure 4C), argyrin B forms three hydrogen-bonding

interactions with Gly47, Gly129 and Ser130. The remaining interactions are VdW with amino acids Thr1, Ser96, Ser116, Asp115, Tyr113, Glu117, Ser23, Asn24, Tyr134, Ala32, Asp167 and Tyr169. In this conformation the tryptophan rings of argyrin B are interacting primarily with polar amino acids including, Ser96, Ser116, Asp115, Glu117 and Tyr113 in which the hydroxyl group is facing towards the tryptophan rings.

In *conformation 2* (Figure 4E), argyrin B forms two hydrogen-bonding interactions with Gly47 and Asn24. The remaining interactions are VdW with amino acids Val133, Phe137, Gln33, Ile30, Ala32, Tyr169, Ser130, Gly129, Val128, Thr1, Ala46, Gly98, Glu117, Tyr113. In this second conformation, trp1 of argyrin B is surrounded by residues Tyr169, Ala32, Gln33, Ile30 and Phe137 forming primarily hydrophobic interactions.

The energetics of binding are similar for $\beta 5i$ and $\beta 5c$. In $\beta 5i$, all bonding is based around the Trp moieties whilst no residues strongly interacted at the opposing end of the inhibitor. The tryptophan rings of argyrin B wrapped around Ser46, each forming hydrogen bonds. Argyrin B interacted with residues only from the $\beta 5i$ subunit in the immunoproteasome, whereas conformations within the constitutive proteasome also displayed interactions with nearby subunit chains i.e, Ser23 and Asn24 from the neighbouring $\beta 4$ and Ala32 from $\beta 3$.

Comparing the $\beta 5$ sites of both the human constitutive and immunoproteasomes (Figure S8), they appear to be remarkably conserved amongst key residues that confer chymotrypsin-like activity Ala20, Met45, Ala49 and Cys52 (Huber et al., 2012) however, the substitutions at the key residues, A46S and T128V (from $\beta 5c$ to $\beta 5i$) surrounding Thr1, as well as the

G48C (from $\beta 5c$ to $\beta 5i$) substitution at the S3 pocket, give the $\beta 5i$ site a more polar character and also have a role in defining the shape of the active site (Huber et al., 2012). Keeping this in mind, the A27S substitution enables the formation of the hydrogen bond between argyirin B and S27 at the $\beta 5i$ site, which is not possible with A27 at $\beta 5c$. Overall however, the predicted binding energies of argyirin B are not statistically different over the two $\beta 5$ sites (Table 2).

Discussion

Argyirins are known inhibitors of the constitutive proteasome that bind reversibly at the active site (Loizidou & Zeinalipour-Yazdi, 2014; Loizidou & Zeinalipour-Yazdi, 2014). In this study we showed that argyirin B, inhibits the constitutive proteasome and immunoproteasome non-competitively and shows greater selectivity towards the $\beta 1i$ site of the immunoproteasome with IC_{50} and K_i values at low μM range. Within the immunoproteasome, argyirin B did not show subunit selectivity as both $\beta 5i$ and $\beta 1i$ are inhibited with similar potency. This is potentially advantageous as studies have shown that the cytotoxicity of proteasome inhibitors does not correlate with $\beta 5$ -inhibition and that the simultaneous inhibition with either $\beta 1$ or $\beta 2$ is needed to reduce protein degradation (Britton et al., 2009a; Alexei F. Kisselev, Callard, & Goldberg, 2006; Weyburne et al., 2017). This is further supported by the study of Britton *et al.* who showed that maximal cytotoxicity in cells is achieved when proteasome inhibitors target more than one sites (Britton et al., 2009b). A possible explanation for this is allosteric interactions between active sites in which inactivation of one site by an inhibitor would lead to the other two sites compensating for loss of activity (A. F. Kisselev, Akopian, Castillo, & Goldberg,

1999). To this end, Weyburne *et al.* (Weyburne et al., 2017) showed that co-inhibition of $\beta 2$ enhances the inhibitory activity of FDA approved $\beta 5$ proteasome inhibitors to triple-negative breast cancer cells, by blocking recovery of proteasome activity. These studies support the hypothesis that subunit specific proteasome inhibitors may not lead to clinically useful drugs and that in contrast efforts should be focused on immunoproteasome over proteasome selectivity.

The ability of argyrin B to inhibit all sites of the proteasome has also been documented by Bülow *et al.* (Bülow et al., 2010) who also reported an IC_{50} value for argyrin B at 4.6 nM from MTT cytotoxicity assays in SW-480 colon cancer cells. This assay measures overall metabolic activity to reflect cell viability and therefore also reflects the overall effect of inhibition of all proteasome sites. In other words, argyrin B inhibits more than one sites of the proteasome leading to a synergistic effect of each active site inhibition and an overall lower IC_{50} value (4.6 nM). In this project, the possibility of synergistic inhibition could not be evaluated, as the inhibition of each active site was determined independently which also explains the higher IC_{50} values that are observed in this study (Table 1). A strong correlation has been observed between theoretical and experimental studies. Molecular modelling predicts that argyrin B will bind the strongest to $\beta 1i$, followed by $\beta 5i$, $\beta 5c$ and last to $\beta 1c$, this trend is also confirmed from the inhibition kinetics experiments (Table 2). Argyrin B interacts with the $\beta 1i$ and $\beta 5i$ sites of the immunoproteasome with higher affinity than the corresponding sites of the constitutive proteasome. In the case of the immunoproteasome, binding is facilitated by additional hydrogen bonding compared to the constitutive

proteasome and this was made possible due to either a better fit within the active site (the case for $\beta 1i$) or an amino acid variation from constitutive to immunoproteasome, A27S for the case of $\beta 5i$.

Taken together, these results further highlight the feasibility of designing immunoproteasome selective inhibitors facilitated by molecular modeling. At the same time, the identification of a non-competitive reversible inhibitor of the immunoproteasome with selectivity towards $\beta 1i$ shows great promise for the development of therapeutics associated with reduced toxicity.

Supporting information:

Supporting information includes Michaelis-Menten plots to determine K_m for each active site; Dixon plot; Cornish Bowden plot; Hanes-Wolf plot at $\beta 1i$; BLAST alignments from murine $\beta 1i$ and $\beta 5i$ active sites to human sequence; amino acid substitutions performed to prepare the humanized immunoproteasome models; sequence alignment of human constitutive proteasome and humanised immunoproteasome sites. PDB coordinates of best-docked conformations and catalytic active sites are provided as separate documents.

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Tables:

Table 1. Summary of IC₅₀ and Ki analysis at β 1c, β 1i, β 5c and β 5i. * denotes statistical significance from t-test.

	β 1c	β 1i	β 5c	β 5i
IC ₅₀ (μ M)	146.5*	8.76	8.30	3.54
SE	1.10	1.08	1.07	1.08
95% CI	122.3-175.5	7.6-10.1	7.8-9.4	3.0-4.1
Ki (μM)	>100	5.21	13.85	6.61
SE	-	0.34	0.96	0.49
95% CI	-	4.54-5.89	11.93-15.76	5.63-7.59

Table 2. Comparison of estimated binding energies from molecular modeling and inhibition constants from kinetic assays

	β 1		β 5	
	CP	IP	CP	IP
Lowest binding energy (kcal/mol)	-9.74 (conf.1) -10.12 (conf.2)	-11.83	-10.52 (conf.1) -10.72 (conf.2)	-10.97
Average binding energy (kcal/mol)	-9.81	-11.66	-10.58	-10.73
SE	0.062	0.045	0.027	0.056
Calculated Ki from assays (μM)	>100	5.21	13.85	6.61

Figure legends:

Figure 1. Chemical structure of argyrin B.

Figure 2. Argyrin B IC_{50} plots at $\beta 1c$, $\beta 1i$, $\beta 5c$, $\beta 5i$ sites. Logarithmic argyrin B concentration against percentage control, initial rate velocity. Tested at $[CP]$ and $[IP] = 0.1 \mu g/well$ and $[S] = K_m$ (K_m values: $\beta 1c = 95.4 \mu M$, $\beta 1i = 69.9 \mu M$, $\beta 5c = 72.4 \mu M$, $\beta 5i = 89.8 \mu M$). Non-linear regression analysis with variable hill slope and $1/y^2$ weighting generated IC_{50} values with respective SEM from 3 independent repeats. A) $\beta 1i$ $IC_{50} = 8.76 \mu M \pm 1.08$, $\beta 1c$ $IC_{50} = 146.5 \mu M \pm 1.10$. B) $\beta 5c = 8.30 \mu M \pm 1.07$, $\beta 5i = 3.54 \mu M \pm 1.08$. DMSO solvent controls used where applicable.

Figure 3. Best-docked conformations of argyrin B (shown as stick representation) at the $\beta 1i$ (A and B) and $\beta 1c$ (C-F) active sites. A) Best-docked conformation of argyrin B at $\beta 1i$ active site, enzyme shown as magenta cartoon representation. Hydrogen bonding interactions between argyrin B and amino acids **Thr1**, **Ser21**, **Ser46** and **Ser129** are shown as green dotted lines. B) Best-docked conformation of argyrin B at $\beta 1i$ active site, enzyme is shown as surface representation where colours red, blue, yellow, magenta correspond to oxygen, nitrogen, sulfur and carbon elements; C) Best-docked *conformation 1* of argyrin B at $\beta 1c$ active site, enzyme is shown as teal cartoon representation. Hydrogen bonding interactions between argyrin B and amino acids **Thr1**, **Gly47**, **Thr22** and **Met116** are shown as green dotted lines; D) Best-docked *conformation 1* of argyrin B at $\beta 1c$ active site, enzyme is shown as surface representation where colours red, blue, yellow, teal correspond to oxygen, nitrogen, sulfur and carbon elements. E) Best-docked *conformation 2* of argyrin B at $\beta 1c$ active site, enzyme is shown as teal cartoon representation. Hydrogen bonding interactions between argyrin B and amino acids **Arg35**, **Gly97**, and **Gly128** are shown as green dotted lines; F) Best-docked *conformation 2* of argyrin B at $\beta 1c$ active site, enzyme is shown as surface representation where colours red, blue, yellow, teal correspond to oxygen, nitrogen, sulfur and carbon elements.

Figure 4. Best-docked conformations of argyrin B (shown as stick representation) at the $\beta 5i$ (A and B) and $\beta 5c$ (C-F) active sites. A) Best-docked conformation of argyrin B at $\beta 5i$ active site, enzyme shown as light blue cartoon representation. Hydrogen bonding interactions between argyrin B and amino acids **Thr1**, **Ser21** and **Ser46** are shown as green dotted lines. B) Best-docked conformation of argyrin B at $\beta 5i$ active site, enzyme is shown as surface representation where colours red, blue, yellow, light blue correspond to oxygen, nitrogen, sulfur and carbon elements; C) Best-docked *conformation 1* of argyrin B at $\beta 5c$ active site, enzyme is shown as light pink cartoon representation. Hydrogen bonding interactions between argyrin B and amino acids **Gly47**, **Gly129** and **Ser130** are shown as green dotted lines; D) Best-docked *conformation 1* of argyrin B at $\beta 5c$ active site, enzyme is shown as surface representation where colours red, blue, yellow, light pink correspond to oxygen, nitrogen, sulfur and carbon elements. E) Best-docked *conformation 2* of argyrin B at $\beta 5c$ active site, enzyme is shown as light pink cartoon representation. Hydrogen bonding interactions

between argyrin B and amino acids **Asn24** and **Gly47** are shown as green dotted lines; F) Best-docked *conformation 2* of argyrin B at $\beta 5c$ active site, enzyme is shown as surface representation where colours red, blue, yellow, light pink correspond to oxygen, nitrogen, sulfur and carbon elements.